

Amendments to the claims:

Please amend claims 1, 3-13, 15, 28, 29 and 33, as follows:

1. (Currently Amended) A composition comprising a substantially purified ~~thermostable~~ AviIII peptide, said AviIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme having at least 70% identity to SEQ ID NO. 3 and a carbohydrate binding domain (CBD) III, the catalytic domain GH74_Ace having a sequence identical to SEQ ID NO 3 in each conserved position marked by an asterisk (*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III

(AviIII_Ace):

GH74 Ace	ATTQPYTWSNVAIGGGG-FVDGIVFNEGAPGILYVRTDIGGMYRWDAANGRWIPLLDWVG
AviIII Aac	AASQAYTWKNVVTGGGGGFTPGIVFNPSAKGVAYARTDIGGAYRLNSDD-TWTPLMDWVG
	*:::*****.*****.*****.**:*****.***:::*****
GH74 Ace	WNNWGYNGVVSIAADPINTNKVWAAVGMYTNSWDPNDGAILRSSDQATWQITPLPFKLG
AviIII Aac	NDTWHDWGIDALATDPVDTDRVYVAVGMYTNEWDPNVGSILRSTDQGDWTETKLPFKVG
	::*:*:::*****:*****.*****.*****.***.*:*****
GH74 Ace	GNMPGRGMGERLAVDPNNDNILYFGAPSGKGLWRSTDSGATWSQMTNFPDVGTYIANPTD
AviIII Aac	GNMPGRGMGERLAVDPNKNLSILYFGARSGHGLWKSTDYCATWSNVTSFTWTGTTFQDSSS
	*****:*****.*****.*****.*****:*****.*****:***
GH74 Ace	TTGYQSDIQGVVWVAFDKSSSSSLGQASKTIFVGVDPPNPVFSRGGATWQAVPGAP-T
AviIII Aac	T--YTSDPVGIAWTFDSTSGSSGSATPRI FVGVDAGKSVFSEDAGATWAWVSGEPQY
	* ** * *:*****:*****.*****.*****.*****.*****.***
GH74 Ace	GFIPHKGVFDPVNHVLIATSN TG GPYDGS S G DVWKF SVTSGTWTRISPVPSTDTANDYF
AviIII Aac	GF LPHKGVLSPEEKTLYISYANGAGPYDGTNGTVHKYNITSGVWTDISP---TSLASTYY
	*****:*****:*****.*****.*****.*****.*****.***
GH74 Ace	GYSGLTIDRQHPNTIMVATQISWVPDIIIFRSTDGGATWTRIDWTSYPNRSRLRYVLDIS
AviIII Aac	GYGLSVDLQVPGTLMVAALNCWNPDELIFRSTDGATWSPIEWNGYPSINYYSYDIS
	*****:*****.*****.*****.*****.*****.*****.***
GH74 Ace	AEPWLTFGVQPNPPVPSPKLGWDEAMAIDPFNSDRMLYGTGATLYATNDLTKWDSGGQI
AviIII Aac	NAPWIQDTTSTDQFP--VRVGWMVEALAI DPFDSNHWLYGTGLTVYGGHDLTNWDSKHN
	:::***:*****.*****.*****.*****.*****.***
GH74 Ace	HIAPMVKGLEETAVNDLISPPSGAPLISALGDLGGFTHADVTAVPSTIFTSPVFTTGTSTV
AviIII Aac	TVKSLAVGIEEMAVLGLITPPGGPALLSAVGDDGGFYHSDLDAPNQAYHTPTYGTTNGI
	:::*****.*****.*****.*****.*****.*****.***
GH74 Ace	DYAE LNPSII VRAGSFDPSQPNDRHVAFSTDGGKNWFQSGEPGGVTGGTVAASADGSR
AviIII Aac	DYAGNKPSNIVRSGASDDYP----TLALSSNFGSTWYADYAASSTGTGVALSADGDT
	:**:*****.*****.*****.*****.*****.***
GH74 Ace	FVWAPGDPGQPVVYAVGFGNSWAASQGV PANAQIRSDRVNPKTFYALSNGTFYRSTDGGV
AviIII Aac	VLLMSSTSGALVSKSQG---TLTAVSSLP SGAVIASDKSDNTVFYGGSGAGIYVSKNTAT
	:::*****:*****.*****.*****.*****.*****.***
GH74 Ace	TFQPVAAGLPSSGAVGMFHAVPGKEGDLWLAASSGLYHSTNGGSSWSAI-TGVSSAVNV
AviIII Aac	SFTKTVS-LGSSTTVNAIR-AHPSIAGDVWASTDKGLWHSTDYGSTFTQIGSGVTAGWSF
	:*:::*****:*****.*****.*****.*****.*****.***

GH74 Ace	GFGKSAPGSSYPVAVFVVTIGGVTGAYRSDDCGTTWVLINDDQHGYGN-WGQAITGDHAN
AviIII Aac	GFGKASSTGSYVVIYGFFTIDGAAGLFKSEDAGTNWQVISDASHGFGSGSANVVNGDLQT
	****::: .** .::: .**.*:* :*:*.*** :*. * .*: .:..** .

GH74 Ace	LRRVYIGTNGRGIVYGDIGGAPSG
AviIII Aac	YGRVFRGHERPGHLLRQSOREPAG
	**:* : * : : *:*

2. (Currently Amended) The composition of claim 1 wherein the ~~thermostable~~ AviIII peptide is further defined as comprising a linker and a signal sequence.
3. ~~(Cancelled) The composition of claim 1 or 2 wherein the glycosyl hydrolase family 74 enzyme catalytic domain of the thermostable AviIII peptide is further defined as having a length of about 730 to about 760 amino acids.~~
4. (Currently Amended) The composition of claim ~~1, 2, or 3~~ 1 or 2 wherein the carbohydrate binding domain (CBD) III of the ~~thermostable~~ AviIII peptide is further defined as comprising a length of about 80 to about 150 amino acids.
5. (Currently Amended) The composition of claim ~~1, 2, or 3~~ 1 or 2 wherein the carbohydrate binding domain (CBD) III of the ~~thermostable~~ AviIII peptide is further defined as comprising a length of about 90 amino acids.
6. (Currently Amended) The composition of claim ~~3~~ 1 wherein the glycosyl hydrolase family 74 enzyme catalytic domain is further defined as including a polypeptide sequence ~~of~~ identical to SEQ ID NO: 3.
7. (Currently Amended) The composition of claim ~~3~~ 1 wherein the carbohydrate binding domain (CBD) III is further defined as a polypeptide sequence of SEQ ID NO: 4.
8. (Previously Amended) The composition of claim ~~3~~ 1 wherein the carbohydrate-binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 5.

9. (Currently Amended) The composition of claim 1 wherein said AviIII protein comprises sequences identical to the polypeptides represented by of-SEQ ID NO: 3 and SEQ ID NO: 4.

10. (Currently Amended) The composition of claim 1, ~~wherein said AviIII protein is encoded by a nucleic acid sequence having the catalytic domain GH74 Ace including at least about 80-90% sequence identity to the polynucleotide sequence of SEQ ID NO: 23.~~

11. (Currently Amended) The composition of claim 1 ~~wherein said AviIII protein is encoded by a nucleic acid sequence having the catalytic domain GH74 including at least about 80% sequence identity to the polynucleotide sequence of SEQ ID NO: 23.~~

12. (Previously Amended) An isolated ~~thermostable~~ AviIII peptide having a polypeptide sequence of SEQ ID NO: 1.

13. (Cancelled)

14. (Currently Amended) An industrial mixture suitable for degrading cellulose, such mixture comprising the ~~thermostable~~ AviIII polypeptide of claim 1.

15. The industrial mixture of claim 14 further defined as comprising a detergent.

Claims 16-27 (cancelled)

28. (Currently Amended) An isolated polypeptide molecule comprising at least one polypeptide sequence selected for the group consisting of:

- a) a polypeptide sequence of SEQ ID NO: 3;
- b) a polypeptide sequence of SEQ ID NO: 4;
- c) a polypeptide sequence of SEQ ID NO: 5;

- d) a polypeptide sequence of SEQ ID NO: 1; and
- e) combinations thereof ~~a polypeptide sequence of SEQ ID NO: 3; SEQ ID NO: 4;~~
~~and SEQ ID NO: 5; or~~
- ~~—— f) a sequence having at least about 70% sequence identity with the polypeptide~~
~~sequence of a), b), c), d), or e).~~

29. (Cancelled)

30. A fusion protein comprising the polypeptide of claim 28 and a heterologous peptide.

31. The fusion protein of claim 30, wherein the heterologous peptide is a substrate targeting moiety.

32. The fusion protein of claim 30, wherein the heterologous peptide is a peptide tag.

33. (Previously Amended) The fusion protein of claim 32, wherein the peptide tag is 6-His, thioredoxin, hemagglutinin, glutathione S-transferase, or OmpA signal sequence tag.

34. The fusion protein of claim 30, wherein the heterologous peptide is an agent that promotes polypeptide oligomerization.

35. The fusion protein of claim 34, wherein the agent is a leucine zipper.

36. A cellulase-substrate complex comprising the isolated polypeptide molecule of claim 28 bound to cellulose.

43. A composition comprising the polypeptide molecule of claim 28 and a carrier.

37-42 (Cancelled)

44-46